Amendments to the Specification:

Please delete the paragraph at page 3, lines 2-20 of the specification and substitute in its place the following amended paragraph:

Carbon fixation, or the conversion of CO2 to reduced forms amenable to cellular biochemistry, occurs by several metabolic pathways in diverse organisms. The most familiar of these is the Calvin Cycle (or "Calvin-Benson" cycle), which is present in cyanobacteria and their plastid derivatives (i.e., chloroplasts), as well as in proteobacteria. The Calvin Cycle utilizes, e.g., the enzyme ~~rubisco~~ Rubisco (ribulose-1,5-bisphosphate carboxylase/oxygenase). Rubisco exists in at least two forms: form I ~~rubisco~~ Rubisco is found in proteobacteria, cyanobacteria, and plastids, e.g., as an octo-dimer compound of eight large subunits, and eight small subunits; form II rubisco is a dimeric form of the enzyme, e.g., as found in proteobacteria. Form I ~~rubisco~~ Rubisco is encoded by two genes (rbcL and rbcS,) which form II ~~rubisco~~ Rubisco has clear similarities to the large subunit of form I ~~rubisco~~ Rubisco, and is encoded by a single gene, also called rbcL. The evolutionary origin of the small subunit of form I ~~rubisco~~ Rubisco remains uncertain; it is less highly conserved than the large subunit, and may have cryptic homology to a portion of the form II protein. *See*, e.g., ~~http://www.blc.arizona.edu/courses/181gh/rick/photosynthesis/Calvin.html, or~~ Raven et al. (1981) The Biology of Plants, 3rd Edition Worth Publishers, Inc. NY, NY for a discussion of the Calvin Cycle. Because of the abundance of Rubisco in Chloroplasts (at about 15% of total protein), it is often indicated to be the most abundant protein on the earth (Raven et al., *id.*).

Please delete the paragraph at page 3, lines 21-28 of the specification and substitute in its place the following amended paragraph:

All photosynthetic organisms catalyze the fixation of atmospheric CO_2 by the bifunctional enzyme ribulose 1,5-bisphosphate carboxylase/oxygenase ("Rubisco"; EC 4.1.1.39). Significant variations in kinetic properties of this enzyme are found among various phylogenetic groups. Because of the abundance and fundamental importance of Rubisco, the enzyme has been extensively studied. Well over 1,000 different Rubisco homologues are available in the public literature (e.g., over 1,000 different Rubisco homologues are ~~listen~~ listed in GenBank alone), and the crystal structure of Rubisco has been solved for several variants of the protein.

Please delete the paragraph beginning at page 82, line 9 and ending at page 83, line 2 and substitute in its place the following amended paragraph:

BLAST is described in Altschul et al., J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information ~~(http://www.ncbi.nlm.nih.gov/)~~ at its ncbi.nlm.nih.gov website. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always>0) and N (penalty score for mismatching residues; always<0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).